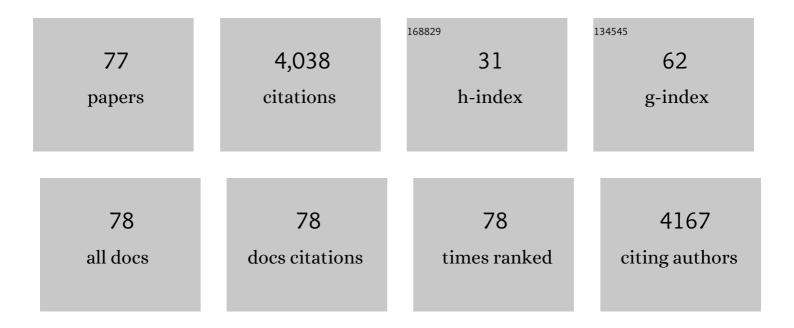
## Hans A Heus

List of Publications by Year in descending order

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HANG & HEUS

#	Article	IF	CITATIONS
1	Improving Breast Cancer Treatment Specificity Using Aptamers Obtained by 3D Cell-SELEX. Pharmaceuticals, 2021, 14, 349.	1.7	16
2	Multivalent Sgc8c-aptamer decorated polymer scaffolds for leukemia targeting. Chemical Communications, 2021, 57, 2744-2747.	2.2	12
3	Ramified rolling circle amplification for synthesis of nucleosomal DNA sequences. Analytical Biochemistry, 2020, 588, 113469.	1.1	12
4	Transcription and Translation in Cytomimetic Protocells Perform Most Efficiently at Distinct Macromolecular Crowding Conditions. ACS Synthetic Biology, 2020, 9, 2797-2807.	1.9	39
5	Dissipative adaptation in driven self-assembly leading to self-dividing fibrils. Nature Nanotechnology, 2018, 13, 849-855.	15.6	160
6	Biomimetic Stress Sensitive Hydrogel Controlled by DNA Nanoswitches. Biomacromolecules, 2017, 18, 3310-3317.	2.6	31
7	A membrane-anchored aptamer sensor for probing IFNÎ <sup>3</sup> secretion by single cells. Chemical Communications, 2017, 53, 8066-8069.	2.2	58
8	DNAâ€Responsive Polyisocyanopeptide Hydrogels with Stress‣tiffening Capacity. Advanced Functional Materials, 2016, 26, 9075-9082.	7.8	42
9	Stable isotope labeling methods for DNA. Progress in Nuclear Magnetic Resonance Spectroscopy, 2016, 96, 89-108.	3.9	15
10	Protein Synthesis in Coupled and Uncoupled Cell-Free Prokaryotic Gene Expression Systems. ACS Synthetic Biology, 2016, 5, 1433-1440.	1.9	17
11	Cellâ€Like Nanostructured Environments Alter Diffusion and Reaction Kinetics in Cellâ€Free Gene Expression. ChemBioChem, 2016, 17, 228-232.	1.3	18
12	Macromolecular crowding creates heterogeneous environments of gene expression in picolitre droplets. Nature Nanotechnology, 2016, 11, 191-197.	15.6	123
13	Macromolecular Crowding in the Cytosol: Underappreciated or Overestimated?. Biophysical Journal, 2015, 108, 114a.	0.2	0
14	Enzymatic preparation of multimilligram amounts of pure single-stranded DNA samples for material and analytical sciences. Analytical Biochemistry, 2015, 475, 68-73.	1.1	17
15	Associative Interactions in Crowded Solutions of Biopolymers Counteract Depletion Effects. Journal of the American Chemical Society, 2015, 137, 13041-13048.	6.6	55
16	Production of Homogeneous Recombinant RNA Using a tRNA Scaffold and Hammerhead Ribozymes. Methods in Molecular Biology, 2015, 1316, 33-44.	0.4	1
17	DNA-functionalized hydrogels for confined membrane-free in vitro transcription/translation. Lab on A Chip, 2014, 14, 2651.	3.1	44
18	Structural and thermodynamic signatures that define pseudotriloop RNA hairpins. Rna, 2013, 19, 1833-1839.	1.6	7

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19	Enhanced transcription rates in membrane-free protocells formed by coacervation of cell lysate. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11692-11697.	3.3	282
20	Fast production of homogeneous recombinant RNA—towards large-scale production of RNA. Nucleic Acids Research, 2012, 40, e102-e102.	6.5	54
21	Force spectroscopy of Rev-peptide–RRE interaction from HIV-1. Soft Matter, 2012, 8, 2103-2109.	1.2	8
22	Unusual Loop-Sequence Flexibility of the Proximal RNA Replication Element in EMCV. PLoS ONE, 2011, 6, e24818.	1.1	2
23	Atomic force microscope-based single-molecule force spectroscopy of RNA unfolding. Analytical Biochemistry, 2011, 414, 1-6.	1.1	27
24	Network theory approach for data evaluation in the dynamic force spectroscopy of biomolecular interactions. Europhysics Letters, 2010, 89, 68004.	0.7	2
25	1H and 13C resonance assignments of a guanine sensing riboswitch's terminator hairpin. Biomolecular NMR Assignments, 2010, 4, 89-91.	0.4	1
26	Enzymatic stereospecific preparation of fluorescent S-adenosyl-l-methionine analogs. Analytical Biochemistry, 2010, 396, 280-283.	1.1	29
27	Functional analysis of the SRV-1 RNA frameshifting pseudoknot. Nucleic Acids Research, 2010, 38, 7665-7672.	6.5	24
28	Preparation of selective and segmentally labeled single-stranded DNA for NMR by self-primed PCR and asymmetrical endonuclease double digestion. Nucleic Acids Research, 2009, 37, e114-e114.	6.5	10
29	The structure–function relationship of the enterovirus 3′-UTR. Virus Research, 2009, 139, 209-216.	1.1	59
30	Cartilage–hair hypoplasia-associated mutations in the RNase MRP P3 domain affect RNA folding and ribonucleoprotein assembly. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 455-466.	1.9	25
31	Multiple segmental and selective isotope labeling of large RNA for NMR structural studies. Nucleic Acids Research, 2008, 36, e89-e89.	6.5	45
32	Breaking pseudo-twofold symmetry in the poliovirus 3'-UTR Y-stem by restoring Watson-Crick base pairs. Rna, 2007, 13, 781-792.	1.6	14
33	Ligand-induced folding of the guanine-sensing riboswitch is controlled by a combined predetermined–induced fit mechanism. Rna, 2007, 13, 2202-2212.	1.6	75
34	An RNA conformational shift in recent H5N1 influenza A viruses. Bioinformatics, 2007, 23, 272-276.	1.8	38
35	Nonspecific Protein Adsorption at the Single Molecule Level Studied by Atomic Force Microscopy. Langmuir, 2007, 23, 9921-9923.	1.6	35
36	Macroscopic Hierarchical Surface Patterning of Porphyrin Trimers via Self-Assembly and Dewetting. Science, 2006, 314, 1433-1436.	6.0	311

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37	Chemical synthesis of picornaviral protein primers of RNA replication. Organic and Biomolecular Chemistry, 2006, 4, 3576.	1.5	11
38	Structural and functional integrity of the coxsackievirus B3 oriR: spacing between coaxial RNA helices. Journal of General Virology, 2006, 87, 689-695.	1.3	15
39	A GCUA tetranucleotide loop found in the poliovirus oriL by in vivo SELEX (un)expectedly forms a YNMG-like structure: Extending the YNMG family with GYYA. Rna, 2006, 12, 1671-1682.	1.6	16
40	AFM Studies of β-Sheet Block Copolymers at Solid Surfaces: High-Resolution Structures and Aggregation Dynamics. Australian Journal of Chemistry, 2006, 59, 560.	0.5	1
41	Structures of Non-Canonical Tandem Base Pairs in RNA Helices: Review. ChemInform, 2004, 35, no.	0.1	0
42	Novel application of sRNA: Stimulation of ribosomal frameshifting. Rna, 2004, 10, 1702-1703.	1.6	30
43	Structures of Non-canonical Tandem Base Pairs in RNA Helices: Review. Nucleosides, Nucleotides and Nucleic Acids, 2003, 22, 559-571.	0.4	14
44	Structure of the Pyrimidine-rich Internal Loop in the Poliovirus 3′-UTR: The Importance of Maintaining Pseudo-2-fold Symmetry in RNA Helices Containing Two Adjacent Non-canonical Base-pairs. Journal of Molecular Biology, 2003, 331, 759-769.	2.0	20
45	Solution structure of the pseudoknot of SRV-1 RNA, involved in ribosomal frameshifting 1 1Edited by I. Tinoco. Journal of Molecular Biology, 2001, 310, 1109-1123.	2.0	102
46	Title is missing!. Helvetica Chimica Acta, 2000, 83, 1278-1289.	1.0	14
47	Solution structure of a HNA–RNA hybrid. Chemistry and Biology, 2000, 7, 719-731.	6.2	66
48	Structure of the ribozyme substrate hairpin of Neurospora VS RNA: A close look at the cleavage site. Rna, 2000, 6, 1821-1832.	1.6	43
49	Title is missing!. Journal of Biomolecular NMR, 1998, 12, 423-433.	1.6	16
50	Structure of the 3'-hairpin of the TYMV pseudoknot: preformation in RNA folding. EMBO Journal, 1998, 17, 7498-7504.	3.5	11
51	New developments in structure determination of pseudoknots. Biopolymers, 1998, 48, 137-153.	1.2	48
52	NMR Structure of a Classical Pseudoknot: Interplay of Single- and Double-Stranded RNA. Science, 1998, 280, 434-438.	6.0	148
53	The detailed structure of tandem G·A mismatched base-pair motifs in RNA duplexes is context dependent. Journal of Molecular Biology, 1997, 271, 147-158.	2.0	53
54	RNA aptamers. Nature Structural Biology, 1997, 4, 597-600.	9.7	14

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55	The structure of the isolated, central hairpin of the HDV antigenomic ribozyme: novel structural features and similarity of the loop in the ribozyme and free in solution. EMBO Journal, 1997, 16, 3685-3692.	3.5	24
56	Unambiguous Structure Characterization of a DNAâ^'RNA Triple Helix by15N- and13C-Filtered NOESY Spectroscopyâ€. Biochemistry, 1996, 35, 1733-1739.	1.2	15
57	A Network of Heterogeneous Hydrogen Bonds in GNRA Tetraloops. Journal of Molecular Biology, 1996, 264, 968-980.	2.0	360
58	Sequential backbone assignment of uniformly 13C-labeled RNAs by a two-dimensional P(CC)H-TOCSY triple resonance NMR experiment. Journal of Biomolecular NMR, 1995, 5, 82-86.	1.6	38
59	Irradiated [15N]DNA as an Internal Standard for Analysis of Base-Oxidized DNA Constituents by Isotope Dilution Mass Spectrometry. Analytical Chemistry, 1995, 67, 399-404.	3.2	5
60	Assignment Strategies and Analysis of Cross-Peak Patterns and Intensities in the Three-Dimensional Homonuclear TOCSY-NOESY of RNA. Journal of Magnetic Resonance Series B, 1994, 103, 134-141.	1.6	28
61	Sequential Backbone Assignment in 13C-Labeled RNA via Through-Bond Coherence Transfer Using Three-Dimensional Triple Resonance Spectroscopy (1H,13C,31P) and Two-Dimensional Hetero TOCSY. Journal of the American Chemical Society, 1994, 116, 4983-4984.	6.6	59
62	Novel proton NMR assignment procedure for RNA duplexes. Journal of the American Chemical Society, 1991, 113, 4360-4361.	6.6	49
63	Nuclear magnetic resonance studies of the hammerhead ribozyme domain. Journal of Molecular Biology, 1991, 217, 113-124.	2.0	110
64	Structural features that give rise to the unusual stability of RNA hairpins containing GNRA loops. Science, 1991, 253, 191-194.	6.0	649
65	Conformational and thermodynamic effects of naturally occurring base methylations in a ribosomal RNA hairpin of Bacillus stearothermophilus. FEBS Journal, 1990, 188, 275-281.	0.2	9
66	Sequence-dependent structural variations of hammerhead RNA enzymes. Nucleic Acids Research, 1990, 18, 1103-1108.	6.5	80
67	ls there a special function for U Â∙ G basepairs in ribosomal RNA?. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1990, 1050, 14-17.	2.4	20
68	The 3′ Terminal Colicin Fragment ofEscherichia coli16S Ribosomal RNA. Conformational Details Revealed by Enzymic and Chemical Probing. Journal of Biomolecular Structure and Dynamics, 1988, 5, 951-963.	2.0	3
69	[12] Isolation and characterization of colicin fragments of bacterial 16S ribosomal RNA. Methods in Enzymology, 1988, 164, 188-200.	0.4	0
70	Circular dichroism and 500-MHz proton magnetic resonance studies of the interaction of Escherichia coli translational initiation factor 3 protein with the 16S ribosomal RNA 3' cloacin fragment. Biochemistry, 1986, 25, 2770-2777.	1.2	23
71	Phylogeny of the conserved 3′ terminal structure of the RNA of small ribosomal subunits. Nucleic Acids Research, 1984, 12, 2595-2604.	6.5	97
72	High-resolution proton magnetic resonance studies of the 3′-terminal colicin fragment of 16 S ribosomal RNA from Escherichia coli. Journal of Molecular Biology, 1983, 170, 939-956.	2.0	31

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73	The Conformation of a Conserved Stem-Loop Structure in Ribosomal RNA. Journal of Biomolecular Structure and Dynamics, 1983, 1, 371-381.	2.0	9
74	Calorimetric measurements of the destabilisation of a ribosomal RNA hairpin by dimethyiation of two adjacent adenosines. Nucleic Acids Research, 1983, 11, 203-210.	6.5	21
75	16S Ribosomal RNA of Escherichia coll contains a N2-methylguanosine at 27 nucleotides from the 3′ end. Nucleic Acids Research, 1981, 9, 2717-2725.	6.5	25
76	Destabilization of secondary structure in 16S ribosomal RNA by dimethylation of two adjacent adenosines. Nucleic Acids Research, 1981, 9, 4413-4422.	6.5	31
77	Adenosine dimethylation of 16S ribosomal RNA: effect of the methylgroups on local conformational stability as deduced from electrophoretic mobility of RNA fragments in denaturing polyacrylamide gels. Nucleic Acids Research, 1981, 9, 267-275.	6.5	21